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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/931,457	08/16/2001	Saverio Carl Falco	BB1116 US CIP	3268

23906 7590 02/09/2006

E I DU PONT DE NEMOURS AND COMPANY
LEGAL PATENT RECORDS CENTER
BARLEY MILL PLAZA 25/1128
4417 LANCASTER PIKE
WILMINGTON, DE 19805

EXAMINER

BAUM, STUART F

ART UNIT	PAPER NUMBER
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1638

DATE MAILED: 02/09/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/931,457	FALCO ET AL.	
	Examiner	Art Unit	
	Stuart F. Baum	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 11 August 2005.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 16 and 18-25 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 16 and 18-25 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☒ The specification is objected to by the Examiner.
- 10) ☒ The drawing(s) filed on 22 February 2002 is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|---|--|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413) |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | Paper No(s)/Mail Date. _____ |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152) |
| Paper No(s)/Mail Date _____ | 6) <input checked="" type="checkbox"/> Other: <u>sequence search results (2)</u> . |

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DETAILED ACTION

RCE Acknowledgment

1. The request filed on 8/11/2005 for a Request for Continued Examination (RCE) under 37 C.F.R. § 1.114, based on parent Application No. 09/931,457 is acceptable and a RCE has been established. An action on the RCE follows.

2. Claims 16, and 18-25 including SEQ ID NO:30 encoding SEQ ID NO:31 are pending and are examined in the present office action.

3. In the "Response After Allowance" filed 8/11/2005, Applicant requested that the filing date of the instant application be changed back to 8/16/2001 from 2/22/2002.

The Office has changed the filing date back to 8/16/2001, and a corrected filing receipt will be mailed to Applicant.

4. In the "Response After Allowance," filed 8/11/2005, applicant also requested the Office to charge the extension of time fee for the prior (parent) application number 09/424,976. MPEP 201.06(c)(X. Extensions of Time) provides that "[i]f an extension of time is necessary to establish continuity between the prior application and the continuing application filed under 37 CFR 1.53(b), the petition for an extension of time must be filed as a separate paper directed to the prior nonprovisional application." (Emphasis added.)

Applicant states that the instant application was filed in response to a restriction requirement made in prior application number 09/424,976 and provided a fee authorization for the extension of time with the filing papers of the instant application (09/931,457). Applicant,

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however, failed to file the fee authorization for the extension of time as a separate paper directed to the prior application. The Office cannot use the fee authorization filed in the instant application to charge the extension of time fee required in the prior application. Accordingly, the prior application was abandoned prior to the filing of the instant application. This means there is no copendency between this application and the prior application and the benefit claims to the prior application. This means that the claimed benefit to the provisional application is not proper. Therefore, the effective priority date of the instant application is 8/16/2001.

In order for this application to claim the benefit of nonprovisional application 09/424,976 and provisional applications 60/065,385 and 60/049,406, Applicant is required to file a petition to revive prior application 09/424,976 for the purposes of copendency. Applicant may use form PTO/SB/64 for filing the petition.

Specification

5. The first paragraph of the specification is objected to because Applicant's priority statement is incorrect, as discussed above.

Claim Rejections - 35 USC § 102

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

6. Claims 16, and 18-25 are rejected under 35 U.S.C. 102(b) as being anticipated by Falco et al (December, 1998, WO 98/56935).

The claims are drawn to an isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide having cysteine synthase activity, wherein the polypeptide has an amino

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acid sequence of at least 95% sequence identity to SEQ ID NO:31, or the full length complement, or wherein the amino acid sequence comprises SEQ ID NO:31, or wherein the nucleotide sequence comprises SEQ ID NO:30; a vector comprising said polynucleotide, a recombinant DNA construct comprising said polynucleotide operably linked to at least one regulatory element, or a method of transforming a cell comprising said polynucleotide, or a cell comprising the recombinant DNA construct, or a plant or seed comprising said recombinant DNA construct.

Falco et al disclose a polynucleotide comprising a nucleotide sequence encoding SEQ ID NO:31, which exhibits 100% sequence identity with SEQ ID NO:31 from the instant application (see enclosed sequence search results) wherein said nucleotide sequence comprises SEQ ID NO:30 (page 6, lines 7-10). SEQ ID NO:30 from WO 98/56935 exhibits 100% sequence identity with SEQ ID NO:30 of the instant application (see enclosed sequence search results). Falco et al disclose transforming monocot or dicot cells with said nucleotide sequence wherein said nucleotide sequence is subcloned into a construct comprising a promoter located 5' and a terminator located 3' to said nucleotide sequence, wherein said construct is inserted into a transformation vector that is used to transform either monocot or dicot cells, which are eventually regenerated into whole plants (pages 23-26, Example 3-4). Falco et al discloses transformed plant or plant seeds comprising said nucleotide sequence (page 27, Example 5) and as such, Falco et al anticipate the claimed invention.

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Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

7. Claim 23 is rejected under 35 USC 101 because the claimed invention is directed to non-statutory subject matter.

The claim recites “A cell comprising” which reads on a human being. Amending the claim to recite “An isolated cell” will obviate the rejection.

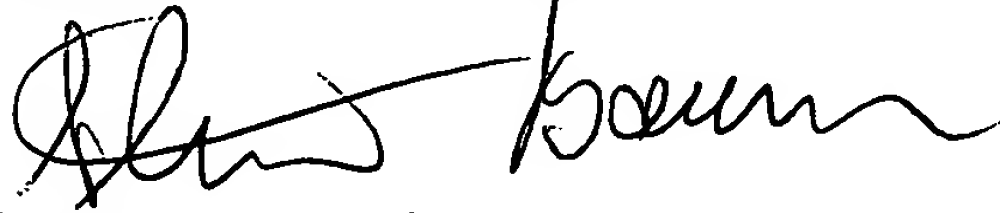
8. No claims are allowed.

9. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Stuart F. Baum whose telephone number is 571-272-0792. The examiner can normally be reached on M-F 8:30-5:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anne Marie Grunberg can be reached at 571-272-0975. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

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Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 571-272-1600.

A handwritten signature in black ink, appearing to read "Stuart F. Baum". The signature is fluid and cursive, with the first name "Stuart" written in a more compact, looped style and the last name "Baum" written in a more extended, flowing style.

Stuart F. Baum Ph.D.

Patent Examiner

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January 30, 2006

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 21, 2004, 20:33:12 ; Search time 530 Seconds
(without alignments)
2605.027 Million cell updates/sec

Title: US-09-931-457A-31
Perfect score: 1623
Sequence: 1 MAVERSGIAKOVTELIGKTP.....LSSVLFSVRREASMTTPEP 325

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Listing first 45 summaries

Post-processing: Minimum Match 0
Maximum Match 100%
Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO.spool/US09931457/runat 18052004 121728 20289/app_query.fasta_1.519
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09931457 @CGN 1 1 470 @runat 18052004 121728 20289 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -PGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:
1: Geneseqn1980s:
2: Geneseqn1990s:
3: Geneseqn2000s:
4: Geneseqn2001as:
5: Geneseqn2001bs:
6: Geneseqn2002s:
7: Geneseqn2003as:
8: Geneseqn2003bs:
9: Geneseqn2003cs:
10: Geneseqn2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1					Aav99906 Fragment
2					Aaq44450 Cysteine
3					Adc76317 DNA homol
4					Aac42360 Arabidops
5					Abz13088 Arabidops
6					Ada68423 Arabidops
7					Ada69412 Rice Gene
8					Ada70437 Rice gene

9	1300	73.0	1179	72.6	1303	3	AAC47965	Spinach c
10	1192	73.0	1179	72.6	1303	3	AAC47965	Abz12294 Arabidops
11	1192	73.0	1179	72.6	1303	3	AAC47965	Abz12294 Arabidops
12	1192	73.0	1179	72.6	1303	3	AAC47965	Aac40774 Arabidops
13	1192	73.0	1179	72.6	1303	3	AAC47965	Abz12690 Arabidops
14	1192	73.0	1179	72.6	1303	3	AAC47965	Aac45719 Arabidops
15	1192	73.0	1179	72.6	1303	3	AAC47965	Aac41206 Arabidops
16	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
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19	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
20	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
21	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
22	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
23	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
24	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
25	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
26	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
27	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
28	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
29	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
30	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
31	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
32	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
33	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
34	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
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36	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
37	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
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39	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
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43	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
44	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops
45	1192	73.0	1179	72.6	1303	3	AAC47965	Aac47965 Arabidops

ALIGNMENTS

RESULT 1
AAV99906
ID AAV99906 standard; cDNA; 1362 BP.
XX AC AAV99906;
XX DT 27-SEP-1999 (first entry)
XX DE Fragment of cysteine synthase gene.
XX KW Biosynthesis; biosynthetic pathway; lysine; threonine; methionine;
XX KW cysteine; isoleucine; amino acid; homoserine kinase;
XX KW aspartic semialdehyde dehydrogenase; diaminopimelate decarboxylase;
XX KW cysteine synthase; cystathione beta-lyase; gene expression; screening;
XX KW inhibition; ss.
XX OS Glycine max.
XX FH Key
XX CDS
XX FT 90..1067
XX FT /tag= a
XX FT /product= "Cysteine synthase fragment"

XX PN W09856935-A2.
XX PD 17-DEC-1998.
XX PP 11-JUN-1998; 98WO-US012073.
XX PR 12-JUN-1997; 97US-0049406P.
XX PR 12-NOV-1997; 97US-0065385P.

PA (DUPO) DU PONT DE NEMOURS & CO E I.
PI Falco SC, Allen SM, Thorpe CJ;
XX WPI; 1999-080910/07.
DR P-PSDB; AAW81018.
XX
XX New isolated plant amino acid biosynthetic enzyme nucleic acids - which
PT encode aspartic semialdehyde dehydrogenase, diaminopimelate
PT decarboxylase, homoserine kinase, cysteine synthase and cystathionine
PT beta-lyase.
XX
XX Claim 17; Page 57-58; 80pp; English.
XX
XX Organisation of the pathway leading to plant biosynthesis of lysine,
CC threonine, methionine, cysteine and isoleucine suggests that over-
CC expression or reduction of expression of genes encoding enzymes involved
CC in that biosynthetic pathway could be used to alter the level of these
CC amino acids in human food and animal feed. This may increase the
CC nutritional quality of human food and animal feed by increasing the
CC production and accumulation of specific free amino acids. The enzymes
CC include aspartic semialdehyde dehydrogenase, homoserine kinase,
CC diaminopimelate decarboxylase, cysteine synthase and cystathionine beta-
CC lyase. The nucleic acids encoding these enzymes can be used for altering
CC the level of expression of the enzymes and for evaluating compounds for
CC their ability to inhibit the enzymes' activity
XX
XX Sequence 1362 BP; 388 A; 243 C; 330 G; 401 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 3.25e-151 Length: 1362
Score: 1623.00 Matches: 325
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-931-457A-31 (1-325) x AAV99906 (1-1362)

QY 1 MetAlaValGluArgSerGlyLeuAlaValThrGluLeuLeuGlyLysThrPro 20
DB 90 ATGGCTGTGAAAGGTCGGAATGCCAAGATGTTACGAATGATGGTAAACCCCA 149
QY 21 LeuValTyrLeuAsnLysLeuAlaAspGlyCysValAlaArgValAlaLysLeuGlu 40
DB 150 TTAGTATATCTAAATAACTTCCGATGGTGTGTTCCCGGTTGCTGCTAACTGGAG 209
QY 41 LeuMetGluProCysSerValLysAspArgGlyTyrSerMetIleAlaAspAla 60
DB 210 TTGATGAGCCCATCTCTAGTGTGAAGCAGCAGATGGGTATGATGATGCTGATGCA 269
QY 61 GluGluLysGlyLeuIleThrProGlyLysSerValLeuIleGluProThrSerGlyAsn 80
DB 270 GAAGAGAGGGGACTTATACACCTGGAAGAGTGTCTCATTGAGCCCAACAGTGGTAAT 329
QY 81 ThrGlyLysGlyLeuAlaPheMetAlaAlaArgGlyTyrLysLeuIleThrMet 100
DB 330 ACTGGCATGGATAGCTTCTATGGCAGCAGCGGGGTTCAAGCTCATATATCAATG 389
QY 101 ProAlaSerMetSerLeuGluArgArgIleLeuLeuAlaPheGlyAlaGluLeuVal 120
DB 390 CCTGCTCTATGAGTCTTGAGAGAGAGATCAATCTATTAGCTTTTGGAGCTGAGTTGGTT 449
QY 121 LeuThrAspProAlaLysGlyMetLysGlyAlaValGlnLysAlaGluGluLeuAla 140
DB 450 CTGACAGATCTCTGTAAGGATGAAGGTTCTGTTTCAAGAGCTGAGAGATATGGCT 509
QY 141 LysThrProAsnAlaTyrIleLeuGlnGlnPheGluAsnProAlaAsnProLysValHis 160
DB 510 AAGACGCCCAATGCCTACATCTTCAACATTTGAACACCTGCTCCCAATCCCAAGTTTCAT 569
QY 161 TyrGluThrThrGlyProGluIleThrLysGlySerAspGlyLysIleAspAlaPheVal 180

DB 570 TATGAACCACTGGTCCAGAGATATGGAAGGCTCCGATGGGAAATTTGATGATTTGTT 629
QY 181 SerGlyIleGlyThrGlyGlyThrIleThrGlyValaGlyLysThrLeuLysGluGlnAsn 200
DB 630 TCTGGGATAGGCACTGGTGTACATAAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 689
QY 201 ProAsnIleLysLeuIleGlyValGluProValGluSerProValLeuSerGlyGlyLys 220
DB 690 CCGAATATTAAGCTGATTTGTTGGAACCACTTGAAGTCCAGTCTCTCAGGAGGAAG 749
QY 221 ProGlyProHisLysIleGlyIleGlyIleGlyAlaGlyPheIleProGlyValLeuGluVal 240
DB 750 CCTGGTCCACACAGATTCAGGGGATTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 809
QY 241 AsnLeuLeuAspGluValValGlnIleSerSerSerSerSerSerSerSerSerSerSer 260
DB 810 AATCTTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 869
QY 261 LeuAlaLysGlyGlyLeuPheValGlyIleSerSerSerSerSerSerSerSerSerSer 280
DB 870 CTTGGCTTAAAGAGGCTTATTTGTGGGATATCTTCCGAGCTGCGAGCTGCTGCTGCT 929
QY 281 PheGlnIleAlaLysArgProGluAsnAlaGlyLysLeuIleValAlaValPheProSer 300
DB 930 TTTGAGATTGCAAAAGACCAAGAAATGCCGGGAGCTTATTTGTTGCTGCTGCTGCTGCT 989
QY 301 PheGlyGluArgTyrLeuSerSerValLeuPheGluSerValArgGluAlaGluSer 320
DB 990 TTGGGGGAGAGGTACCTGCTCTCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1049
QY 321 MetThrPheGluPro 325
DB 1050 ATGACCTTTGAGCCC 1064
RESU 2
AAQ4 50
ID AQ44450 standard; cDNA to mRNA; 1303 BP.
XX AC Q44450;
XX DT OCT-1994 (first entry)
XX DE Cysteine synthase.
XX KW Cysteine synthase; plant; expression; probe; ss.
XX OS Spinach oleraceae.
XX FH Location/Qualifiers
XX CDS 52..1029
XX JP06038770-1 /tag= a
XX 15-FEB-1994.
XX 05-FEB-1992; 2JJP-00020315.
XX 05-FEB-1992; 2JJP-00020315.
XX (MITS) MITSUBISHI CORP.
XX (MITU) MITSUBISHI CASEI CORP.
XX WPI; 1994-094834/12.
XX P-PSDB; AAR49830.
XX Novel gene coding cysteine synthase - used to increase the cysteine
XX content of an agricultural plant.
XX Claim 2; Page 4-6; 6pp; Japanese.
XX The cysteine content in an agricultural product can be increased by
XX expressing the cysteine synthase in a plant. Probes V822 and V812 used in

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2004, 07:37:59 ; Search time 653 Seconds
(without alignments)
8860.713 Million cell updates/sec

Title: US-09-931-457A-30
Perfect score: 1362
Sequence: 1 actttgtagttcgttagtag.....aaaaaaaaaaaaaaaaaaaa 1362

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1362	100.0	1362	2	AAV99906 Fragment
					Aac42360 Arabidops
					Aac44450 Cysteine
					Adc76317 DNA homol
					Abz13088 Arabidops
					Ada68423 Arabidops
					Ada69412 Rice gene
					Ada70437 Rice gene
					Aag74413 Spinach c
					Aac34662 Arabidops
					Aac33559 Arabidops
					Adc64221 Thalecres
					Aac44727 Arabidops
					Aac45323 Arabidops
					Add17591 DNA (SeqI
					Aac47965 Arabidops
					Aac40774 Arabidops
					Abz12690 Arabidops
					Aac45719 Arabidops
					Abz12294 Arabidops
					Aac41206 Arabidops
					Aac44993 Arabidops
					Add17590 DNA (SeqI

24	425	31.2	683	9	ADC75696	DNA homol
25	419	30.8	1037	9	ADC76318	DNA homol
26	416.2	30.6	918	3	AAC41635	Arabidops
27	415.6	30.5	1006	9	ADC75697	DNA homol
28	408.2	30.0	614	9	ADC75699	DNA homol
29	408.2	30.0	614	9	ADD16770	DNA (SeqI
30	383.2	28.1	933	9	ADD16769	DNA (SeqI
31	381.6	28.0	913	9	ADC76310	DNA homol
32	375.8	27.6	657	8	ACL17131	DNA clone
33	369	27.1	894	9	ADC76316	DNA homol
34	369	27.1	1431	3	ADD16773	DNA (SeqI
35	360.2	26.4	618	8	AAC46837	Arabidops
36	358.8	26.3	1200	7	ADA69647	Rice gene
37	357.6	26.3	1417	3	AAC51477	Arabidops
38	356.2	26.2	1481	3	AAC47004	Arabidops
39	356.2	26.2	1579	4	ABA01246	O-acetyls
40	337.4	24.8	1779	3	AAC51458	Arabidops
41	337.2	24.8	506	8	ACL17123	DNA clone
42	335.2	24.6	528	7	ABX57527	Arabidops
43	333	24.4	506	9	ADD16772	DNA (SeqI
44	330.4	24.4	675	8	ACL17144	DNA clone
45						

ALIGNMENTS

RESULT 1
AAV99906
ID AAV99906 standard; cDNA; 1362 BP.
AC AAV99906;
DT 27-SEP-1999 (first entry)
DE Fragment of cysteine synthase gene.
KW Biosynthesis; biosynthetic pathway; lysine; threonine; methionine;
KW cysteine; isoleucine; amino acid; homoserine kinase;
KW aspartic semialdehyde dehydrogenase; diaminopimelate decarboxylase;
KW cysteine synthase; cystathione beta-lyase; gene expression; screening;
KW inhibition; ss.
OS Glycine max.
PH Key
FT CDS
FT Location/Qualifiers
FT 90..1067
FT /*tag= a
FT /product= "Cysteine synthase fragment"

WO9856935-A2.
17-DEC-1998.
11-JUN-1998; 98WO-US012073.
12-JUN-1997; 97US-0049406P.
12-NOV-1997; 97US-0065385P.
(DUPO) DU PONT DE NEMOURS & CO E I.
Falco SC, Allen SM, Thorpe CJ;
WPI; 1999-080910/07.
P-PSDB; AAW81018.
New isolated plant amino acid biosynthetic enzymes nucleic acids - which
encode aspartic semialdehyde dehydrogenase, diaminopimelate
decarboxylase, homoserine kinase, cysteine synthase and cystathionine
beta-lyase.
Claim 17; Page 57-58; 80pp; English.

CC Organisation of the pathway leading to plant biosynthesis of lysine,
CC threonine, methionine, cysteine and isoleucine suggests that over-
CC expression or reduction of expression of genes encoding enzymes involved
CC in that biosynthetic pathway could be used to alter the level of these
CC amino acids in human food and animal feed. This may increase the
CC nutritional quality of human food and animal feed by increasing the
CC production and accumulation of specific free amino acids. The enzymes
CC include aspartic semialdehyde dehydrogenase, homoserine kinase,
CC diaminopimelate decarboxylase, cysteine synthase and cystathione beta-
CC lyase. The nucleic acids encoding these enzymes can be used for altering
CC the level of expression of the enzymes and for evaluating compounds for
CC their ability to inhibit the enzymes' activity
XX

SQ Sequence 1362 BP; 388 A; 243 C; 330 G; 401 T; 0 U; 0 Other;

Query Match 100.0%; Score 1362; DB 2; Length 1362;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTTTGAGTTCGTAGATAGCCGATGCTGCTTGTCTTAGTGTGCTCAGTCAATTCCTGTTCT 60
DB |||||
QY 61 CAACTCAAGCTTTGTAGTACAGATATATATGCTGTTGAAAGTCCGGAATTCGCAAG 120
DB |||||
QY 121 ATGTTACGGAAATGATTTGTTGTAAGCCCAATAGTATATCTAATAAATCTTCCGATGTT 180
DB |||||
QY 181 GTGTTCCCGGGTGTCTGCTAACTGGAGTTGATGGAGCCATGCTCTAGTGTGAGGACA 240
DB |||||
QY 241 GGATTTGGGTATAGTATGATGCTGATGCGAGAGAGAGGAGGACTTATCACACCTCGAAGA 300
DB |||||
QY 301 GTGTCCTCATTGAGCCCAAGTGGTAAATCTGCTAGTGGCAATGGATTAGCCTTCATGGCAGCAG 360
DB |||||
QY 361 CCAGGGGTACAAAGCTCATAATTAACAATGCTGCTTCTATGAGTCTTGAAGAGAAATCA 420
DB |||||
QY 421 TTCTATTAGCTTTTGGAGCTGAGTGGTCTGACAGATCCTGCTAAGGGAATGAAGGTG 480
QY 481 CTGTTCAAGAGGCTGAAGAGATATTTGGCTAAGACGCCCAATGCTTACATATCTTCAACAAT 540
DB |||||
QY 541 FTGAAACCTGCTCAATCCCAAGGTTCAITATGAACCACTGGTCCAGAGATATGGAAG 600
DB |||||
QY 601 GCTCCGATGGGAAATTTGATGCAATTTGTTCTGGATAGGCACTGGTGGTACAAATACAG 660
DB |||||
QY 661 GTGCTGGAATATCTTAAAGAGCAGATCCGATATTAAGCTGATGGTGGTGGACCCAG 720
DB |||||
QY 721 TTGAAAGTCCAGTCTCTCAGGAGGAAAGCCTGCTCACACAGATTCAGGGATTTGGTG 780
DB |||||
QY 781 CTGTTTATCCCTGGTGTCTTGAAGTCAATCTTCTTGAAGTGTGTTCAATATCA 840
DB |||||

DB 781 CTGTTTATCCCTGGTGTCTTGAAGTCAATCTTCTTGAAGTGTGTTCAATATCA 840
QY 841 GTGATGAAGCAATAGAACTGCAAGCTTCTTGGCTTAAAGAGGCTTATTTGTGGAA 900
DB |||||
QY 841 GTGATGAAGCAATAGAACTGCAAGCTTCTTGGCTTAAAGAGGCTTATTTGTGGAA 900
QY 901 TATCTTCCGGAGCTGCAGCTGCTGCTGCTTTTTCAGATTGCAAAAGACCAAGAAATGCG 960
DB |||||
QY 901 TATCTTCCGGAGCTGCAGCTGCTGCTGCTTTTTCAGATTGCAAAAGACCAAGAAATGCG 960
QY 961 GGAAGCTTATTTGTTGCTGCTTTTCCAGCTTCCGGAGAGGTTACTGCTCCTCGTGTAT 1020
DB |||||
QY 961 GGAAGCTTATTTGTTGCTGCTTTTCCAGCTTCCGGAGAGGTTACTGCTCCTCGTGTAT 1020
QY 1021 TTGAGTCAGTGAGACCGCAAGCTGAAAGCATGTTTGGAGCCCTGAATTCCTGTTAAG 1080
DB |||||
QY 1021 TTGAGTCAGTGAGACCGCAAGCTGAAAGCATGTTTGGAGCCCTGAATTCCTGTTAAG 1080
QY 1081 GCTCTCACTACTGAATTTTCTTGTACTTGTACCAGGCTTTAACTAGATTGTTAGAGTAC 1140
DB |||||
QY 1081 GCTCTCACTACTGAATTTTCTTGTACTTGTACCAGGCTTTAACTAGATTGTTAGAGTAC 1140
QY 1141 TACTGTTGTGACTCTGACTCTTAAATTAATAAATGCTTCCAAAGACCTAGTTTCTTGTAT 1200
DB |||||
QY 1141 TACTGTTGTGACTCTGACTCTTAAATTAATAAATGCTTCCAAAGACCTAGTTTCTTGTAT 1200
QY 1201 GCTCTGAGCGATAATTTTGTGCTGCAACATTAATAAAGTATTCAAAGTGTCTTATAAG 1260
DB |||||
QY 1201 GCTCTGAGCGATAATTTTGTGCTGCAACATTAATAAAGTATTCAAAGTGTCTTATAAG 1260
QY 1261 TAACATGTTTCATCTTTTGTGTTGTTGAGACGAAACCGATGAGTCTAATATCTATGT 1320
DB |||||
QY 1261 TAACATGTTTCATCTTTTGTGTTGTTGAGACGAAACCGATGAGTCTAATATCTATGT 1320
QY 1321 TTCTGATTTCTTCTTGTAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 1362
DB |||||
QY 1321 TTCTGATTTCTTCTTGTAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 1362

RESULT 2

AC42360
AAC42360 standard; DNA; 1120 BP.

AC AC42360;

DT OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 35256.

KW Hybridization assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.

OS Arabidopsis thaliana.

PN EP1033405-A2

PD 06-SEP-2000.

XX 25-FEB-2000; 2000-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-012548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-012624P.

XX 29-MAR-1999; 99US-012678P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

XX 16-APR-1999; 99US-0129845P.

XX 19-APR-1999; 99US-0130077P.

XX 21-APR-1999; 99US-0130449P.